



323-100USD.ST25

SEQUENCE LISTING

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Nasoff, Marc S.  
Prince, Alfred M.

<120> METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT VIRAL ANTIGENS

<130> 323-100USD

<140> 10/677,956

<141> 2003-10-01

<150> 08/931,855

<151> 1997-09-16

<150> 08/563,733

<151> 1995-11-08

<150> 08/272,271

<151> 1994-07-08

<150> 07/616,369

<151> 1990-11-21

<150> 07/573,643

<151> 1990-08-27

<160> 71

<170> PatentIn version 3.3

<210> 1

<211> 795

<212> DNA

<213> Human immunodeficiency virus

<220>

<221> CDS

<222> (16)..(789)

<400> 1

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Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val  
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cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99

His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
15 20 25

gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147

Glu Gln Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
30 35 40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195

Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
45 50 55 60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243

323-100USD.ST25

Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu		
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gaa	gct	gca	gaa	tgg	gat	aga	gtg	cat	cca	gtg	cat	gca	ggg	cct	att	291	
Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile		
			80					85					90				
gca	cca	ggc	cag	atg	aga	gaa	cca	agg	gga	agt	gac	ata	gca	gga	act	339	
Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr		
		95					100					105					
act	agt	acc	ctt	cag	gaa	caa	ata	gga	tgg	atg	aca	aat	aat	cca	cct	387	
Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro		
	110					115					120						
atc	cca	gta	gga	gaa	att	tat	aaa	aga	tgg	ata	atc	ctg	gga	tta	aat	435	
Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn		
125					130					135					140		
aaa	ata	gta	aga	atg	tat	agc	cct	acc	agc	att	ctg	gac	ata	aga	caa	483	
Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln		
				145					150					155			
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Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr		
			160					165					170				
cta	aga	gcc	gag	caa	gct	tca	cag	gag	gta	aaa	aat	tgg	atg	aca	gaa	579	
Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu		
		175					180					185					
acc	ttg	ttg	gtc	caa	aat	gcg	aac	cca	gat	tgt	aag	act	att	tta	aaa	627	
Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys		
	190					195					200						
gca	ttg	gga	cca	gcg	gct	aca	cta	gaa	gaa	atg	atg	aca	gca	tgt	cag	675	
Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln		
205					210					215					220		
gga	gta	gga	gga	ccc	aaa	aat	caa	caa	tta	tta	tcc	tta	tgg	ggg	tgt	723	
Gly	Val	Gly	Gly	Pro	Lys	Asn	Gln	Gln	Leu	Leu	Ser	Leu	Trp	Gly	Cys		
				225					230					235			
aaa	ggg	aaa	ctt	gtt	tgt	tat	act	tcc	gtt	aaa	tgg	aat	gga	ccc	ggc	771	
Lys	Gly	Lys	Leu	Val	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly		
			240					245					250				
cat	aag	gca	aga	gtt	ttg	taataa										795	
His	Lys	Ala	Arg	Val	Leu												
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 <213> Human immunodeficiency virus

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323-100USD.ST25

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala  
20 25 30

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala  
35 40 45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln  
50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu  
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln  
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu  
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly  
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg  
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu  
145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
210 215 220

Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu  
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Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg  
245 250 255

Val Leu

<210> 3  
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<220>  
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 <222> (16)..(789)

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                   1                  5                  10

cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99  
 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
                   15                  20                  25

gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147  
 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
                   30                  35                  40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195  
 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
                   45                  50                  55                  60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243  
 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu  
                   65                  70                  75

gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291  
 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile  
                   80                  85                  90

gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act 339  
 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr  
                   95                  100                  105

act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct 387  
 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro  
                   110                  115                  120

atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat 435  
 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn  
                   125                  130                  135                  140

aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa 483  
 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln  
                   145                  150                  155

gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act 531  
 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr  
                   160                  165                  170

cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa 579  
 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu  
                   175                  180                  185

acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa 627  
 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys  
                   190                  195                  200

## 323-100USD.ST25

gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag	675
Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln	
205 210 215 220	
gga gta gga gga ccc aaa aat caa caa aga tta aat tta tgg ggg tgt	723
Gly Val Gly Gly Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys	
225 230 235	
aaa ggg aaa ctt att tgt tat act tcc gtt aaa tgg aat gga ccc ggc	771
Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly	
240 245 250	
cat aag gca aga gtt ttg taataa	795
His Lys Ala Arg Val Leu	
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Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile
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Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
20 25 30

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
35 40 45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
 165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
 180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
 195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
 210 215 220

Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu  
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Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg  
 245 250 255

Val Leu

<210> 5  
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 <213> Human immunodeficiency virus

<220>  
 <221> CDS  
 <222> (16)..(789)

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cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99  
 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
 15 20 25

gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147  
 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
 30 35 40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195  
 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
 45 50 55 60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243  
 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu  
 65 70 75

gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291  
 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile  
 Page 6

323-100USD.ST25

80										85					90					
gca	cca	ggc	cag	atg	aga	gaa	cca	agg	gga	agt	gac	ata	gca	gga	act	339				
Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr					
		95					100					105								
act	agt	acc	ctt	cag	gaa	caa	ata	gga	tgg	atg	aca	aat	aat	cca	cct	387				
Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro					
	110					115					120									
atc	cca	gta	gga	gaa	att	tat	aaa	aga	tgg	ata	atc	ctg	gga	tta	aat	435				
Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn					
125					130					135					140					
aaa	ata	gta	aga	atg	tat	agc	cct	acc	agc	att	ctg	gac	ata	aga	caa	483				
Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln					
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gga	cca	aag	gaa	ccc	ttt	aga	gac	tat	gta	gac	cgg	ttc	tat	aaa	act	531				
Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr					
			160					165					170							
cta	aga	gcc	gag	caa	gct	tca	cag	gag	gta	aaa	aat	tgg	atg	aca	gaa	579				
Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu					
		175					180					185								
acc	ttg	ttg	gtc	caa	aat	gcg	aac	cca	gat	tgt	aag	act	att	tta	aaa	627				
Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys					
	190					195					200									
gca	ttg	gga	cca	gcg	gct	aca	cta	gaa	gaa	atg	atg	aca	gca	tgt	cag	675				
Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln					
205					210					215					220					
gga	gta	gga	gga	cca	caa	aat	caa	caa	ctt	tta	aat	tta	tgg	ggg	tgt	723				
Gly	Val	Gly	Gly	Pro	Gln	Asn	Gln	Gln	Leu	Leu	Asn	Leu	Trp	Gly	Cys					
				225					230					235						
aga	ggg	aaa	gct	att	tgt	tat	act	tcc	gtt	caa	tgg	aat	gga	ccc	ggc	771				
Arg	Gly	Lys	Ala	Ile	Cys	Tyr	Thr	Ser	Val	Gln	Trp	Asn	Gly	Pro	Gly					
			240					245					250							
cat	aag	gca	aga	gtt	ttg	taataa										795				
His	Lys	Ala	Arg	Val	Leu															
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<210> 6  
 <211> 258  
 <212> PRT  
 <213> Human immunodeficiency virus

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Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala  
 20 25 30

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala  
 Page 7

35

40

45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln  
50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu  
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln  
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu  
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly  
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg  
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu  
145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
210 215 220

Pro Gln Asn Gln Gln Leu Leu Asn Leu Trp Gly Cys Arg Gly Lys Ala  
225 230 235 240

Ile Cys Tyr Thr Ser Val Gln Trp Asn Gly Pro Gly His Lys Ala Arg  
245 250 255

Val Leu

<210> 7  
<211> 378  
<212> DNA  
<213> Hepatitis C virus



## 323-100USD.ST25

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&lt;222&gt; (16)..(375)

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cgt aac acc aac cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt 99  
 Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly  
 15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147  
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu  
 30 35 40

ggt gtg cgc gcg acg agg aag act tcc gag cgg tcg caa cct cga ggt 195  
 Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly  
 45 50 55 60

aga cgt cag cct atc ccc aag gtg cgt cgg ccg gag ggc agg acc tgg 243  
 Arg Arg Gln Pro Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp  
 65 70 75

gct cag ccc ggg tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg 291  
 Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly  
 80 85 90

tgg gcg gga tgg ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339  
 Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly  
 95 100 105

ccc aca gac ccc cgg cgt agg tcg cgc aat ttg ggt taa 378  
 Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly  
 110 115 120

&lt;210&gt; 8

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Hepatitis C virus

&lt;400&gt; 8

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
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Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60

## 323-100USD.ST25

Ile Pro Lys Val Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly  
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly  
115 120

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Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly  
15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147  
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu  
30 35 40

ggt gtg cgc gcg acg agg aag act tcc gag cgg tcg caa cct cga ggt 195  
Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly  
45 50 55 60

aga cgt cag cct atc ccc aag gca cgt cgg ccc gag ggc agg acc tgg 243  
Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp  
65 70 75

gct cag ccc ggg tac cct tgg ccc ctg tat ggc aat gag ggt tgc ggg 291  
Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly  
80 85 90

tgg gcg gga tgg ctg ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339  
Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly  
95 100 105

ccc aca gac ccc cgg cgt agg tcg cgc aat ttg ggt taa 378  
Pro Thr Asp Pro Arg Arg Ser Arg Asn Leu Gly  
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<210> 10  
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&lt;213&gt; Hepatitis C virus

&lt;400&gt; 10

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly  
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly  
115 120

&lt;210&gt; 11

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Hepatitis C virus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (16)..(375)

&lt;400&gt; 11

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Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys  
1 5 10

cgt aac acc aac cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt 99  
Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly  
15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147  
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu  
30 35 40

ggt gtg cgc gcg acg agg aag act tcc gag cgg tcg caa cct cga ggt 195  
Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly  
45 50 55 60

## 323-100USD.ST25

aga cgt cag cct atc ccc aag gac cgt cgg tcc acg ggc aag tcc tgg 243  
 Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp  
 65 70 75

ggg aag ccc ggg tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg 291  
 Gly Lys Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly  
 80 85 90

tgg gcg gga tgg ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339  
 Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly  
 95 100 105

ccc aca gac ccc cgg cgt agg tcc cgc aat ttg ggt taa 378  
 Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly  
 110 115 120

<210> 12  
 <211> 120  
 <212> PRT  
 <213> Hepatitis C virus

<400> 12

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60

Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly  
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
 100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly  
 115 120

<210> 13  
 <211> 378  
 <212> DNA  
 <213> Hepatitis C virus

<220>

## 323-100USD.ST25

&lt;221&gt; CDS

&lt;222&gt; (16)..(375)

&lt;400&gt; 13

aggagggttt ttcatt atg agc acg aat cct aaa cct caa aga aaa acc aaa 51  
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys  
 1 5 10

cgt aac acc aac cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt 99  
 Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly  
 15 20 25

cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg 147  
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu  
 30 35 40

ggt gtg cgc gcg acg agg aag act tcc gag cgg tcg caa cct cga ggt 195  
 Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly  
 45 50 55 60

aga cgt cag cct atc ccc aag gca cgt cgg tcc gag ggc agg tcc tgg 243  
 Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp  
 65 70 75

gct cag ccc ggg tac cct tgg ccc ctg tat ggc aat gag ggt tgc ggc 291  
 Ala Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly  
 80 85 90

tgg gcg gga tgg ctg ctg tct ccc cgt ggc tct cgg cct agc tgg ggc 339  
 Trp Ala Gly Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly  
 95 100 105

ccc aca gac ccc cgg cgt agg tcg cgc aat ttg ggt taa 378  
 Pro Thr Asp Pro Arg Arg Arg Ser Arg Asn Leu Gly  
 110 115 120

&lt;210&gt; 14

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Hepatitis C virus

&lt;400&gt; 14

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly  
 65 70 75 80

323-100USD.ST25

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly  
115 120

<210> 15  
<211> 381  
<212> DNA  
<213> Hepatitis C virus

<220>  
<221> CDS  
<222> (16)..(378)

<400> 15  
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Met Pro Ile His His His His His His Gly Pro Gly  
1 5 10

tcc gtc act gtg tcc cat cct aac atc gag gag gtt gct ctg tcc acc 99  
Ser Val Thr Val Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr  
15 20 25

acc gga gag atc ccc ttt tac ggc aag gct atc ccc ctc gag gtg atc 147  
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile  
30 35 40

aag ggg gga aga cat ctc atc ttc tgc cac tca aag aag aag tgc gac 195  
Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp  
45 50 55 60

gag ctc gcc gcg aag ctg gtc gca ttg ggc atc aat gcc gtg gcc tac 243  
Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr  
65 70 75

tac cgc ggt ctt gac gtg tct gtc atc ccg acc agc ggc gat gtt gtc 291  
Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val  
80 85 90

gtc gtg tca acc gat gct ctc atg act ggc ttt acc ggc gac ttc gac 339  
Val Val Ser Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp  
95 100 105

tcg gtg ata gac tgc aat acg ggt acc gag ctc gaa ttc taa 381  
Ser Val Ile Asp Cys Asn Thr Gly Thr Glu Leu Glu Phe  
110 115 120

<210> 16  
<211> 121  
<212> PRT  
<213> Hepatitis C virus

<400> 16

323-100USD.ST25

Met Pro Ile His His His His His Gly Pro Gly Ser Val Thr Val  
 1 5 10 15  
 Ser His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile  
 20 25 30  
 Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg  
 35 40 45  
 His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala  
 50 55 60  
 Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu  
 65 70 75 80  
 Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ser Thr  
 85 90 95  
 Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp  
 100 105 110  
 Cys Asn Thr Gly Thr Glu Leu Glu Phe  
 115 120

<210> 17  
 <211> 774  
 <212> DNA  
 <213> Hepatitis C virus

<220>  
 <221> CDS  
 <222> (16)..(771)

<400> 17  
 aggagggttt ttcatt atg tcc cct ata cta ggt tat tgg aaa att aag ggc 51  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly 10  
 ctt gtg caa ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat 99  
 Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr 15 20 25  
 gaa gag cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa 147  
 Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys 30 35 40  
 aag ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat 195  
 Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp 45 50 55 60  
 ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata gct 243  
 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala 65 70 75

323-100USD.ST25

gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca gag att	291
Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile	
	80
	85
	90
tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt gtt tcg aga	339
Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg	
	95
	100
	105
att gca tat agt aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc	387
Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser	
	110
	115
	120
aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa	435
Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys	
	125
	130
	135
	140
aca tat tta aat ggt gat cat gta acc cat cct gac ttc atg ttg tat	483
Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr	
	145
	150
	155
gac gct ctt gat gtt gtt tta tac atg gac cca atg tgc ctg gat gcg	531
Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala	
	160
	165
	170
ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa	579
Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln	
	175
	180
	185
att gat aag tac ttg aaa tcc agc aag tat ata gca tgg cct ttg cag	627
Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln	
	190
	195
	200
ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat	675
Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp	
	205
	210
	215
	220
ctg gtt ccg cgt gga tcc gac gtc aag ttc ccg ggt ggc ggt cag atc	723
Leu Val Pro Arg Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile	
	225
	230
	235
gtt ggt gga gtt tac ttg ttg ccg cgc agg gaa ttc atc gtg act gac	771
Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp	
	240
	245
	250
tga	774

<210> 18  
 <211> 252  
 <212> PRT  
 <213> Hepatitis C virus

<400> 18

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30



323-100USD.ST25

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220

Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val  
225 230 235 240

Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp  
245 250

<210> 19  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 19  
ccaaaattac catatgccaa tcgtgcagaa c 31

<210> 20  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 20  
gacccggcca taaggcaaga gttttgtaat aag 33

<210> 21  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 21  
gatccttatt acaaaactct tgccttatgg ccgg 34

<210> 22  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 22  
gctcgcatat gagcacgatt cccaaacc 28

<210> 23  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 23  
gacgaattct taacccaaatt tgcgcgacct ac 32

<210> 24  
<211> 66  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 24  
gatccgacgt caagttcccg ggtggcggtc agatcgttgg tggagtttac ttgttgccgc 60

gcaggg

66

<210> 25  
 <211> 66  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 25  
 aattccctgc gcggcaacaa gtaaactcca ccaacgatct gaccgccacc cggaacttg 60

acgtcg 66

<210> 26  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 26  
 ggaattccat atgtccccta tactaggt 28

<210> 27  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 27  
 cggaattctc acctgctcgg caacaa 26

<210> 28  
 <211> 52  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 28  
 tatgcctatt catcatcatc atcatcatgg cccgggaatt ctaagtaagt ag 52

<210> 29  
 <211> 54  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 29

gatcctacttt acttagaatt cccgggcat gatgatgatg atgatgaata ggca

54

<210> 30  
 <211> 978  
 <212> DNA  
 <213> non-A, non-B hepatitis virus

<220>  
 <221> CDS  
 <222> (1)..(978)  
 <223> non-A, non-B hepatitis virus structural antigen

<400> 30  
 atg agc acg att ccc aaa cgt caa aga aaa acc aaa cgt aac acc aac 48  
 Met Ser Thr Ile Pro Lys Arg Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

cgt cgc cca cag gac gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt 96  
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30

gga gtt tac ttg ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg 144  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45

acg agg aag act tcc gag cgg tcg caa cct cga ggt aga cgt cag cct 192  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60

atc ccc aag gca cgt cgg ccc gag ggc agg acc tgg gct cag ccc ggg 240  
 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly  
 65 70 75 80

tac cct tgg ccc ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg 288  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95

ctc ctg tct ccc cgt ggc tct cgg cct agc tgg ggc ccc aca gac ccc 336  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
 100 105 110

cgg cgt agg tcg cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc 384  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125

ggc ttc gcc gac ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt 432  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu  
 130 135 140

gga ggc gct gcc agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac 480  
 Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160

ggc gtg aac tat gca aca ggg aac ctt cct ggt tgc tct ttc tct atc 528  
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175

ttc ctt ctg gcc ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac 576  
 Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr  
 180 185 190

323-100USD.ST25

caa gtg cgc aat tcc tcg ggg ctt tac cat gtc acc aat gat tgc cct Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp Cys Pro 195 200 205	624
aac tcg agt gtt gtg tac gag gcg gcc gat gcc atc ctg cac act ccg Asn Ser Ser Val Val Tyr Glu Ala Ala Asp Ala Ile Leu His Thr Pro 210 215 220	672
ggg tgt gtc cct tgc gtt cgc gag ggt aac gcc tcg agg tgt tgg gtg Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser Arg Cys Trp Val 225 230 235 240	720
gcg gtg acc ccc acg gtg gcc acc agg gac ggc aaa ctt ccc aca acg Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Thr Thr 245 250 255	768
cag ctt cga cgt cat atc gat ctg ctt gtc ggg agc gcc acc ctc tgc Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala Thr Leu Cys 260 265 270	816
tcg gcc ctc tac gtg ggg gac ctg tgc ggg tct gtc ttt ctc gtt ggt Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Gly 275 280 285	864
caa ctg ttt acc ttc tct ccc agg cgc cac tgg acg acg caa gac tgc Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Asp Cys 290 295 300	912
aat tgt tct atc tat ccc ggc cat ata acg ggt cat cgc atg gca tgg Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp 305 310 315 320	960
gat atg atg atg aac tgg Asp Met Met Met Asn Trp 325	978

<210> 31  
<211> 948  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a fusion protein that includes sequences from  
glutathione-S-transferase, non-A, non-B hepatitis virus capsid  
antigen, and a Factor X cleavage site

<220>  
<221> CDS  
<222> (1)..(945)

<400> 31 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 1 5 10 15	48
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30	96
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45	144

## 323-100USD.ST25

ggt Gly	ttg Leu	gag Glu	ttt Phe	ccc Pro	aat Asn	ctt Leu	cct Pro	tat Tyr	tat Tyr	att Ile	gat Asp	ggt Gly	gat Asp	gtt Val	aaa Lys	192
50						55				60						
tta Leu	aca Thr	cag Gln	tct Ser	atg Met	gcc Ala	atc Ile	ata Ile	cgt Arg	tat Tyr	ata Ile	gct Ala	gac Asp	aag Lys	cac His	aac Asn	240
65					70					75					80	
atg Met	ttg Leu	ggt Gly	ggt Gly	tgt Cys	cca Pro	aaa Lys	gag Glu	cgt Arg	gca Ala	gag Glu	att Ile	tca Ser	atg Met	ctt Leu	gaa Glu	288
				85					90					95		
gga Gly	gcg Ala	gtt Val	ttg Leu	gat Asp	att Ile	aga Arg	tac Tyr	ggt Gly	gtt Val	tcg Ser	aga Arg	att Ile	gca Ala	tat Tyr	agt Ser	336
			100					105					110			
aaa Lys	gac Asp	ttt Phe	gaa Glu	act Thr	ctc Leu	aaa Lys	gtt Val	gat Asp	ttt Phe	ctt Leu	agc Ser	aag Lys	cta Leu	cct Pro	gaa Glu	384
		115					120					125				
atg Met	ctg Leu	aaa Lys	atg Met	ttc Phe	gaa Glu	gat Asp	cgt Arg	tta Leu	tgt Cys	cat His	aaa Lys	aca Thr	tat Tyr	tta Leu	aat Asn	432
	130					135					140					
ggt Gly	gat Asp	cat His	gta Val	acc Thr	cat His	cct Pro	gac Asp	ttc Phe	atg Met	ttg Leu	tat Tyr	gac Asp	gct Ala	ctt Leu	gat Asp	480
145					150					155					160	
gtt Val	gtt Val	tta Leu	tac Tyr	atg Met	gac Asp	cca Pro	atg Met	tgc Cys	ctg Leu	gat Asp	gcg Ala	ttc Phe	cca Pro	aaa Lys	tta Leu	528
				165					170					175		
gtt Val	tgt Cys	ttt Phe	aaa Lys	aaa Lys	cgt Arg	att Ile	gaa Glu	gct Ala	atc Ile	cca Pro	caa Gln	att Ile	gat Asp	aag Lys	tac Tyr	576
			180					185					190			
ttg Leu	aaa Lys	tcc Ser	agc Ser	aag Lys	tat Tyr	ata Ile	gca Ala	tgg Trp	cct Pro	ttg Leu	cag Gln	ggc Gly	tgg Trp	caa Gln	gcc Ala	624
		195					200					205				
acg Thr	ttt Phe	ggt Gly	ggt Gly	ggc Gly	gac Asp	cat His	cct Pro	cca Pro	aaa Lys	tcg Ser	gat Asp	ctg Leu	atc Ile	gaa Glu	ggt Gly	672
	210					215					220					
cgt Arg	ggg Gly	atc Ile	ccc Pro	aat Asn	tcg Ser	agc Ser	tcg Ser	gta Val	ccc Pro	atg Met	agc Ser	acg Thr	att Ile	ccc Pro	aaa Lys	720
225					230					235					240	
cct Pro	caa Gln	aga Arg	aaa Lys	acc Thr	aaa Lys	cgt Arg	aac Asn	acc Thr	aac Asn	cgt Arg	cgc Arg	cca Pro	cag Gln	gac Asp	gtc Val	768
				245					250					255		
aag Lys	ttc Phe	ccg Pro	ggt Gly	ggc Gly	ggt Gly	cag Gln	atc Ile	gtt Val	ggt Gly	gga Gly	gtt Val	tac Tyr	ttg Leu	ttg Leu	ccg Pro	816
			260					265					270			
cgc Arg	agg Arg	ggc Gly	cct Pro	aga Arg	ttg Leu	ggt Gly	gtg Val	cgc Arg	gcg Ala	acg Thr	agg Arg	aag Lys	act Thr	tcc Ser	gag Glu	864
		275					280					285				
cgg Arg	tcg Ser	caa Gln	cct Pro	cga Arg	ggt Gly	aga Arg	cgt Arg	cag Gln	cct Pro	atc Ile	ccc Pro	aag Lys	gca Ala	cgt Arg	cgg Arg	912

290

295

ccc gag ggc agg acg ggg atc ggg aat tca tcg tga  
Pro Glu Gly Arg Thr Gly Ile Gly Asn Ser Ser  
305 310 315

948

<210> 32  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 32  
atgagcacga ttcccaaacc t

21

<210> 33  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 33  
gaggaagact tccgagc

17

<210> 34  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 34  
gtcctgccct cgggccg

17

<210> 35  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 35  
acccaaattg cgcgacctac g

21

<210> 36  
<211> 19  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 36  
tgggtaaggt catcgatac 19

<210> 37  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 37  
aaggtcatcg ataccct 17

<210> 38  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 38  
agatagagaa agagcaac 18

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 39  
ggaccagttc atcatcatat at 22

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 40  
cagttcatca tcatatccca 20

<210> 41  
<211> 5  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 41



Gly Ile Pro Asn Ser  
1 5

<210> 42  
<211> 15  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for linker protein in GST-NANBV 693-691

<220>  
<221> CDS  
<222> (1)..(15)

<400> 42  
ggg atc ccc aat tca  
Gly Ile Pro Asn Ser  
1 5

15

<210> 43  
<211> 3  
<212> PRT  
<213> Artificial

<220>  
<223> Carboxy-terminal linker protein in GST-NANBV 693-691

<400> 43

Asn Ser Ser  
1

<210> 44  
<211> 12  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for carboxy-terminal linker protein in GST-NANBV 693-691

<220>  
<221> CDS  
<222> (1)..(9)

<400> 44  
aat tca tcg tga  
Asn Ser Ser  
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12

<210> 45  
<211> 9  
<212> PRT  
<213> Artificial

<220>  
<223> Linker protein in GST-NANBV 15-18

&lt;400&gt; 45

Gly Ile Pro Ile Glu Phe Leu Gln Pro  
 1 5

<210> 46  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> CDS  
 <222> (1)..(27)  
 <223> Codes for linker protein in GST-NANBV 15-18

<400> 46  
 ggg atc ccc atc gaa ttc ctg cag ccc  
 Gly Ile Pro Ile Glu Phe Leu Gln Pro  
 1 5

27

<210> 47  
 <211> 7  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Carboxy-terminal linker protein in GST-NANBV 15-18

&lt;400&gt; 47

Trp Gly Ile Gly Asn Ser Ser  
 1 5

<210> 48  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for carboxy-terminal linker protein in GST-NANBV 15-18

<220>  
 <221> CDS  
 <222> (1)..(21)

<400> 48  
 tgg ggg atc ggg aat tca tcg tga  
 Trp Gly Ile Gly Asn Ser Ser  
 1 5

24

<210> 49  
 <211> 8  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Linker protein in GST-NANBV 15-17

&lt;400&gt; 49

Gly Ile Pro Asn Ser Cys Ser Pro  
 1 5

<210> 50  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for linker protein in GST-NANBV 15-17

<220>  
 <221> CDS  
 <222> (1)..(24)

<400> 50  
 ggg atc ccc aat tcc tgc agc cct  
 Gly Ile Pro Asn Ser Cys Ser Pro  
 1 5

24

<210> 51  
 <211> 6  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Carboxy-terminal linker protein in GST-NANBV 15-17

&lt;400&gt; 51

Gly Ile Gly Asn Ser Ser  
 1 5

<210> 52  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for carboxy-terminal linker protein in GST-NANBV 15-17

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 52  
 ggg atc ggg aat tca tgc tga  
 Gly Ile Gly Asn Ser Ser  
 1 5

21

<210> 53  
 <211> 5  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Thrombin cleavage site in GST-NANBV 15-17

<400> 53

Val Pro Arg Gly Ser  
 1 5

<210> 54  
 <211> 15  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for thrombin cleavage site in GST-NANBV 15-17

<220>  
 <221> CDS  
 <222> (1)..(15)

<400> 54  
 gtt ccg cgt gga tcc  
 Val Pro Arg Gly Ser  
 1 5

15

<210> 55  
 <211> 7  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Linker protein in GST-NANBV 15-17

<400> 55

Pro Ser Asn Ser Cys Ser Pro  
 1 5

<210> 56  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for linker protein in GST-NANBV 15-17

<220>  
 <221> CDS  
 <222> (1)..(21)

<400> 56  
 cca tcg aat tcc tgc agc cct  
 Pro Ser Asn Ser Cys Ser Pro  
 1 5

21

<210> 57

<211> 5  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Carboxy-terminal linker protein in GST-NANBV 15-17

<400> 57

Gly Ile His Arg Asp  
 1 5

<210> 58  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for carboxy-terminal linker protein in GST-NANBV 15-17

<220>  
 <221> CDS  
 <222> (1)..(15)

<400> 58  
 gga att cat cgt gac tga  
 Gly Ile His Arg Asp  
 1 5

18

<210> 59  
 <211> 9  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Linker protein in GST-NANBV 690-691

<400> 59

Gly Ile Pro Asn Ser Ser Ser Val Pro  
 1 5

<210> 60  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for linker protein in GST-NANBV 690-691

<220>  
 <221> CDS  
 <222> (1)..(27)

<400> 60  
 ggg atc ccc aat tcg agc tcg gta ccc  
 Gly Ile Pro Asn Ser Ser Ser Val Pro  
 1 5

27

<210> 61  
 <211> 7  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Carboxy-terminal linker protein in GST-NANBV 690-691

<400> 61

Thr Gly Ile Gly Asn Ser Ser  
 1 5

<210> 62  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for carboxy-terminal linker protein in GST-NANBV 690-691

<220>  
 <221> CDS  
 <222> (1)..(21)

<400> 62  
 acg ggg atc ggg aat tca tcg tga 24  
 Thr Gly Ile Gly Asn Ser Ser  
 1 5

<210> 63  
 <211> 66  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 63  
 gatccatgag cacgattccc aaacctcaaa gaaaaaccaa acgtaacacc aaccgtcgcc 60  
 cacagg 66

<210> 64  
 <211> 66  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 64  
 aattcctgtg ggggacggtt ggtgttacgt ttggtttttc tttgaggttt gggaatcgtg 60  
 ctcatg 66

## 323-100USD.ST25

<210> 65  
 <211> 759  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for a fusion protein that includes sequences from glutathione-S-transferase, non-A, non-B hepatitis virus capsid antigen, and a thrombin cleavage site

<220>  
 <221> CDS  
 <222> (1)..(756)

<400> 65  
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac 576  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190

323-100USD.ST25

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc 624  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt 672  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220

gga tcc atg agc acg att ccc aaa cct caa aga aaa acc aaa cgt aac 720  
Gly Ser Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn  
225 230 235 240

acc aac cgt cgc cca cag gaa ttc atc gtg act gac tga 759  
Thr Asn Arg Arg Pro Gln Glu Phe Ile Val Thr Asp  
245 250

<210> 66  
<211> 66  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 66  
gatccgacgt caagttcgcg ggtggcggtc agatcggttg tggagtttac ttgttgccgc 60

gcaggg 66

<210> 67  
<211> 66  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide

<400> 67  
aattccctgc gcggcaacaa gtaaactcca ccaacgatct gaccgccacc cggaacttg 60

acgtcg 66

<210> 68  
<211> 759  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a fusion protein that includes sequences from  
glutathione-S-transferase, non-A, non-B hepatitis virus capsid  
antigen, and a thrombin cleavage site

<220>  
<221> CDS  
<222> (1)..(756)

<400> 68  
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro



323-100USD.ST25  
10

1	5														15	
act Thr	cga Arg	ctt Leu	ctt Leu 20	ttg Leu	gaa Glu	tat Tyr	ctt Leu	gaa Glu 25	gaa Glu	aaa Lys	tat Tyr	gaa Glu 30	gag Glu	cat His	ttg Leu	96
tat Tyr	gag Glu	cgc Arg 35	gat Asp	gaa Glu	ggt Gly	gat Asp	aaa Lys 40	tgg Trp	cga Arg	aac Asn	aaa Lys 45	aag Lys	ttt Phe	gaa Glu	ttg Leu	144
ggt Gly 50	ttg Leu	gag Glu	ttt Phe	ccc Pro	aat Asn	ctt Leu 55	cct Pro	tat Tyr	tat Tyr	att Ile	gat Asp 60	ggt Gly	gat Asp	ggt Val	aaa Lys	192
tta Leu 65	aca Thr	cag Gln	tct Ser	atg Met	gcc Ala 70	atc Ile	ata Ile	cgt Arg	tat Tyr	ata Ile 75	gct Ala	gac Asp	aag Lys	cac His	aac Asn 80	240
atg Met	ttg Leu	ggt Gly	ggt Gly	tgt Cys 85	cca Pro	aaa Lys	gag Glu	cgt Arg	gca Ala 90	gag Glu	att Ile	tca Ser	atg Met	ctt Leu 95	gaa Glu	288
gga Gly	gcg Ala	gtt Val	ttg Leu 100	gat Asp	att Ile	aga Arg	tac Tyr	ggt Gly 105	gtt Val	tcg Ser	aga Arg	att Ile	gca Ala 110	tat Tyr	agt Ser	336
aaa Lys	gac Asp	ttt Phe 115	gaa Glu	act Thr	ctc Leu	aaa Lys	gtt Val 120	gat Asp	ttt Phe	ctt Leu	agc Ser	aag Lys 125	cta Leu	cct Pro	gaa Glu	384
atg Met 130	ctg Leu	aaa Lys	atg Met	ttc Phe	gaa Glu	gat Asp 135	cgt Arg	tta Leu	tgt Cys	cat His	aaa Lys 140	aca Thr	tat Tyr	tta Leu	aat Asn	432
ggt Gly 145	gat Asp	cat His	gta Val	acc Thr	cat His 150	cct Pro	gac Asp	ttc Phe	atg Met	ttg Leu 155	tat Tyr	gac Asp	gct Ala	ctt Leu	gat Asp 160	480
gtt Val	gtt Val	tta Leu	tac Tyr	atg Met 165	gac Asp	cca Pro	atg Met	tgc Cys	ctg Leu 170	gat Asp	gcg Ala	ttc Phe	cca Pro	aaa Lys 175	tta Leu	528
gtt Val	tgt Cys	ttt Phe	aaa Lys 180	aaa Lys	cgt Arg	att Ile	gaa Glu	gct Ala 185	atc Ile	cca Pro	caa Gln	att Ile	gat Asp 190	aag Lys	tac Tyr	576
ttg Leu	aaa Lys	tcc Ser 195	agc Ser	aag Lys	tat Tyr	ata Ile	gca Ala 200	tgg Trp	cct Pro	ttg Leu	cag Gln	ggc Gly 205	tgg Trp	caa Gln	gcc Ala	624
acg Thr	ttt Phe 210	ggt Gly	ggt Gly	ggc Gly	gac Asp	cat His 215	cct Pro	cca Pro	aaa Lys	tcg Ser	gat Asp 220	ctg Leu	gtt Val	ccg Pro	cgt Arg	672
gga Gly 225	tcc Ser	gac Asp	gtc Val	aag Lys	ttc Phe 230	ccg Pro	ggt Gly	ggc Gly	ggt Gly	cag Gln 235	atc Ile	gtt Val	ggt Gly	gga Gly	gtt Val 240	720
tac Tyr	ttg Leu	ttg Leu	ccg Pro	cgc Arg 245	agg Arg	gaa Glu	ttc Phe	atc Ile	gtg Val 250	act Thr	gac Asp	tga				759

## 323-100USD.ST25

<210> 69  
 <211> 32  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 69  
 gaattcttac ctgcgcggca acaagtaaac tc

32

<210> 70  
 <211> 32  
 <212> DNA  
 <213> Artificial

<220>  
 <223> synthetic oligonucleotide

<400> 70  
 gctgatcca gcacgattcc caaacctcaa ag

32

<210> 71  
 <211> 816  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for a fusion protein that includes sequences from  
 glutathione-S-transferase, non-A, non-B hepatitis virus capsid  
 antigen, and a thrombin cleavage site

<220>  
 <221> CDS  
 <222> (1)..(813)

<400> 71  
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
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 1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95

## 323-100USD.ST25

gga Gly	gcg Ala	gtt Val	ttg Leu 100	gat Asp	att Ile	aga Arg	tac Tyr	ggt Gly 105	gtt Val	tcg Ser	aga Arg	att Ile	gca Ala 110	tat Tyr	agt Ser	336
aaa Lys	gac Asp	ttt Phe 115	gaa Glu	act Thr	ctc Leu	aaa Lys	gtt Val 120	gat Asp	ttt Phe	ctt Leu	agc Ser	aag Lys 125	cta Leu	cct Pro	gaa Glu	384
atg Met	ctg Leu 130	aaa Lys	atg Met	ttc Phe	gaa Glu	gat Asp 135	cgt Arg	tta Leu	tgt Cys	cat His	aaa Lys 140	aca Thr	tat Tyr	tta Leu	aat Asn	432
ggt Gly 145	gat Asp	cat His	gta Val	acc Thr	cat His 150	cct Pro	gac Asp	ttc Phe	atg Met	ttg Leu 155	tat Tyr	gac Asp	gct Ala	ctt Leu	gat Asp 160	480
gtt Val	gtt Val	tta Leu	tac Tyr	atg Met 165	gac Asp	cca Pro	atg Met	tgc Cys	ctg Leu 170	gat Asp	gcg Ala	ttc Phe	cca Pro	aaa Lys 175	tta Leu	528
gtt Val	tgt Cys	ttt Phe	aaa Lys 180	aaa Lys	cgt Arg	att Ile	gaa Glu	gct Ala 185	atc Ile	cca Pro	caa Gln	att Ile	gat Asp 190	aag Lys	tac Tyr	576
ttg Leu	aaa Lys	tcc Ser 195	agc Ser	aag Lys	tat Tyr	ata Ile	gca Ala 200	tgg Trp	cct Pro	ttg Leu	cag Gln	ggc Gly 205	tgg Trp	caa Gln	gcc Ala	624
acg Thr	ttt Phe 210	ggt Gly	ggt Gly	ggc Gly	gac Asp	cat His 215	cct Pro	cca Pro	aaa Lys	tcg Ser	gat Asp 220	ctg Leu	gtt Val	ccg Pro	cgt Arg	672
gga Gly 225	tcc Ser	agc Ser	acg Thr	att Ile	ccc Pro 230	aaa Lys	cct Pro	caa Gln	aga Arg	aaa Lys 235	acc Thr	aaa Lys	cgt Arg	aac Asn	acc Thr 240	720
aac Asn	cgt Arg	cgc Arg	cca Pro	cag Gln 245	gac Asp	gtc Val	aag Lys	ttc Phe	ccg Pro 250	ggt Gly	ggc Gly	ggt Gly	cag Gln	atc Ile 255	gtt Val	768
ggt Gly	gga Gly	gtt Val	tac Tyr 260	ttg Leu	ttg Leu	ccg Pro	cgc Arg	agg Arg 265	gaa Glu	ttc Phe	atc Ile	gtg Val	act Thr 270	gac Asp	tga	816